Practitioner's Docket No. <u>MPI01-014P1RNM</u>   *PATENT*

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Curtis, Rory A.J. et al
Application No.:   10/050,216   Group No.:   N/A

Filed: January 16, 2002   Examiner: N/A
For: 46798, A HUMAN MATRIX METALLOPROTEINASE AND USES THEREFOR

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Arlington, VA 22202

SUBMISSION OF "SEQUENCE LISTING," COMPUTER READABLE COPY, AND/OR AMENDMENT PERTAINING THERETO FOR BIOTECHNOLOGY INVENTION CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE

1. [X] This replies to the Notice to File Missing Parts of Nonprovisional Application Dated March 18, 2001.
    Applicant filed a complete paper copy of the sequence listing in the present application. However Applicant inadvertently filed a computer readable form which included an incomplete version of the sequence listing. In this response as set forth below, applicant submits herewith a corrected paper copy of the sequence listing together with a computer readable form which contains the same sequence listing as the corrected paper copy.

    [X] A copy of the Notice to File Missing Parts of Nonprovisional Application is enclosed.

CERTIFICATION UNDER 37 C.F.R. SECTIONS 1.8(a) and 1.10*

I hereby certify that, on the date shown below, this correspondence is being:

MAILING

[X]   deposited with the United States Postal Service in an envelope addressed to the Box Sequence, U.S. Patent and Trademark Office, P.O. Box 2327, Arlington, VA 22202
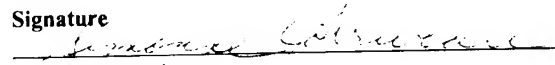
37 C.F.R. SECTION 1.8(a)   **37 C.F.R. SECTION 1.10***

[X]   with sufficient postage as first class mail.   [ ]   as "Express Mail Post Office to Address" Mailing Label No. _____

TRANSMISSION

[ ]   transmitted by facsimile to the Patent and Trademark Office.

Signature
_____
Simonne Corriveau
(*type or print name of person certifying*)

Date: June 14, 2002

***WARNING:** Each paper or fee filed by "Express Mail" **must** have the number of the "Express Mail" mailing label placed thereon prior to mailing. 37 C.F.R. section 1.10(b). "Since the filing of correspondence under section 1.10 without the Express Mail mailing label thereon is an oversight that can be avoided by the exercise of reasonable care, requests for waiver of this requirement will **not** be granted on petition." Notice of Oct. 24, 1996, 60 Fed. Reg. 56,439, at 56,442.*

IDENTIFICATION OF PERSON MAKING STATEMENT

2. I, __Jean M. Silveri_____

    (type or print name of person signing below)

    state the following:

ITEMS BEING SUBMITTED

3. Submitted herewith is/are:

    A. [X] "Sequence Listing(s)" for the nucleotide and/or amino acid sequence(s) in this application. Each "Sequence Listing" is assigned a separate identifier as required in 37 C.F.R. Section 1.821(c) and 37 C.F.R. Sections 1.822 and 1.823.

    B. [ ] An amendment to the description and/or claims, wherein reference is made to the sequence by use of the assigned identifier, as required in 37 C.F.R. Section 1.821(d).

    C. [X] A copy of each "Sequence Listing" submitted for this application in computer readable form, in accordance with the requirements of 37 C.F.R. Sections 1.821(e) and 1.824.

    D. [ ] Please transfer to this application, in accordance with 37 C.F.R. Section 1.821(e), the computer readable copy(ies) from applicant's other application identified as follows:

In re application of:			
Application No.:		Group No.:	
Filed:		Examiner:	
For:			

The Computer readable form(s) of applicant's other application corresponds to the "Sequence Identifier(s)" of the application as follows:

Computer Readable Form   "Sequence Identifier"

(other application)   (this application)

E. [X] A statement that the content of each "Sequence Listing" submitted and each computer readable copy are the same, as required in 37 C.F.R. Section 1.821(g).

    ( ) Because the statement is not made by a person registered to practice before the Office, the Statement is verified as required in 37 C.F.R. Section 1.821(b).

F. [X] Because this submission is made in fulfilling the requirement under 37 C.F.R. Section 1.821(g), a statement that the submission includes no new matter

    ( ) Because the statement is not made by a person registered to practice before the Office, the statement is verified, as required in 37 C.F.R. Section 1.821(g).

STATEMENT THAT "SEQUENCE LISTING" AND COMPUTER READABLE COPY ARE THE SAME AND/OR THAT PAPERS SUBMITTED INCLUDES NO NEW MATTER

4. I hereby state:

A. [X] Each computer readable form submitted in this application, including those forms requested to be transferred from applicant's other application, is the same as the "Sequence Listing" to which it is indicated to relate.

B. [X] All papers accompanying this submission, or for which a request for transfer from applicants' other application, introduce no new matter.

EXTENSION OF TERM

5. The proceedings herein are for a patent application and the provisions of 37 C.F.R. Section 1.136 apply.

    (a) ( ) Applicant petitions for an extension of time under 37 C.F.R. Section 1.136 (fees: 37 C.F.R. Section 1.17(a)(1)-(4)) for the total number of months checked below:

Extension (months)	Fee for other than small entity	Fee for small entity
( ) one month	$ 110.00	$ 55.00
( ) two months	$ 390.00	$ 195.00
( ) three months	$ 890.00	$ 445.00
( ) four months	$1,390.00	$ 695.00

Fee   <u>$0.00</u>

Practitioner's Docket No. MPI01-014P1RNM

If an additional extension of time is required, please consider this a petition therefor.

[ ] An extension for _____ month has already been secured, and the fee paid therefor of _____$0.00_____ is deducted from the total fee due for the total months of extension now requested.

Extension fee due with this request _____$0.00_____

OR

(b) [ ] Applicant believes that no extension of term is required. However, this conditional petition is being made to provide for the possibility that applicant has inadvertently overlooked the need for a petition and fee for extension of time.

FEE PAYMENT

6. [ ] Attached is a check in the sum of $_____.

( ) Charge Account No. _501668_ the sum of _____$0.00_____.
A duplicate of this transmittal is attached.

FEE DEFICIENCY

8. [X] If any additional extension and/or fee is required, charge Account No. _501668_.

June 14, 2002

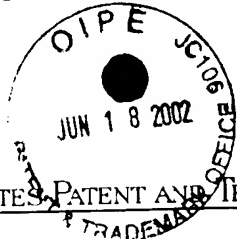MILLENNIUM PHARMACEUTICALS, INC.

By: _____
Jean M. Silveri
Registration No. 39,030
75 Sidney Street
Cambridge, MA 02139
Telephone - 617-679-7336
Facsimile - 617-551-8820

UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON D.C. 20231
www.uspto.gov

APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
10/050,216	01/16/2002	Rory A. J. Curtis	MPI2001-014PTRCP1(M)

CONFIRMATION NO. 6278

FORMALITIES LETTER

OC000000007664551

Millennium Pharmaceuticals, Inc.
75 Sidney Street
Cambridge, MA 02139

Date Mailed: 03/18/2002

NOTICE TO FILE MISSING PARTS OF NONPROVISIONAL APPLICATION

FILED UNDER 37 CFR 1.53(b)

Filing Date Granted

An application number and filing date have been accorded to this application. The item(s) indicated below, however, are missing. Applicant is given **TWO MONTHS** from the date of this Notice within which to file all required items and pay any fees required below to avoid abandonment. Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a).

- The oath or declaration is unsigned.
- To avoid abandonment, a late filing fee or oath or declaration surcharge as set forth in 37 CFR 1.16(l) of $130 for a non-small entity, must be submitted with the missing items identified in this letter.
- **The balance due by applicant is $ 130.**

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

- **For Rules Interpretation, call (703) 308-4216**
- **To Purchase PatentIn Software, call (703) 306-2600**
- **For PatentIn Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov**

A copy of this notice MUST be returned with the reply.

Customer Service Center
Initial Patent Examination Division (703) 308-1202

PART 1 - ATTORNEY/APPLICANT COPY

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: **10/050,216**

Source: **OIPE**

Date Processed by STIC: **2/6/2002**

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
 http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
          Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/050,216

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length

Sequence(s) 7 contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

pp 1-5

**Does Not Comply
Corrected Diskette Needed**

```
 4 <110> APPLICANT: Curtis, Rory A.J., Lora, Jose M.
 6 <120> TITLE OF INVENTION: 46798, A HUMAN MATRIX METALLOPROTEINASE
 7       AND USES THEREFOR
 9 <130> FILE REFERENCE: MPI2001-014P1RCP1(M)
11 <140> CURRENT APPLICATION NUMBER: US/10/050,216
11 <141> CURRENT FILING DATE: 2002-01-16
11 <160> NUMBER OF SEQ ID NOS: 10
13 <170> SOFTWARE: FastSEQ for Windows Version 3.0
```

*Suggestion:
Consult
Sequence Rules
for valid format*

ERRORED SEQUENCES

```
224 <210> SEQ ID NO: 3
225 <211> LENGTH: 1335
226 <212> TYPE: DNA
227 <213> ORGANISM: Homo sapiens
229 <220> FEATURE:
230 <221> NAME/KEY: CDS
231 <222> LOCATION: (1)...(1335)
233 <400> SEQUENCE: 3
```

pp 1-3

```
E--> 234 atg gtc gcg cgc gtc ggc ctc ctg ctg cgc gcc ctg cag ctg cta ctg
     235 Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu Gln Leu Leu Leu
     236  1               5                  10                  15
E--> 238 tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg
     239 Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu
     240                 20                  25                  30
E--> 242 cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa
     243 Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu
     244             35                  40                  45
E--> 246 cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga
     247 Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg
     248         50                  55                  60
E--> 250 gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc
     251 Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg
     252     65                  70                  75                  80
E--> 254 gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc
     255 Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr
     256                 85                  90                  95
E--> 258 aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga
     259 Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg
     260                 100                 105                 110
E--> 262 cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggg ggc
     263 His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly
```

48
96
144

insert cumulative base totals at right margin of each line

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/050,216

DATE: 02/06/2002
TIME: 19:11:09

Input Set : **A:\SEQUENCE LISTING.txt**
Output Set: **N:\CRF3\02062002\J050216.raw**

```
        264           115                    120                    125
E--> 266  gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac
     267  Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp
     268           130                    135                    140
E--> 270  caa gat gag cgc tgg tcc ctg agc cgc cgc cgc ggg cgc aac ctg ttc
     271  Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe
     272  145                    150                    155                    160
E--> 274  gtg gtg ctg gcg cac gag atc ggt cac acg ctt ggc ctc acc cac tcg
     275  Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly Leu Thr His Ser
     276                    165                    170                    175
E--> 278  ccc gcg ccg cgc gcg ctc atg gcg ccc tac tac aag agg ctg ggc cgc
     279  Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg
     280                    180                    185                    190
E--> 282  gac gcg ctg ctc agc tgg gac gac gtg ctg gcc gtg cag agc ctg tat
     283  Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr
     284           195                    200                    205
E--> 286  ggg aag ccc cta ggg ggc tca gtg gcc gtc cag ctc cca gga aag ctg
     287  Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu
     288           210                    215                    220
E--> 290  ttc act gac ttt gag acc tgg gac tcc tac agc ccc caa gga agg cgc
     291  Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg
     292  225                    230                    235                    240
E--> 294  cct gaa acg cag ggc cct aaa tac tgc cac tct tcc ttc gat gcc atc
     295  Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile
     296                    245                    250                    255
E--> 298  act gta gac agg caa cag caa ctg tac att ttt aaa ggg agc cat ttc
     299  Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe
     300                    260                    265                    270
E--> 302  tgg gag gtg gca gct gat ggc aac gtc tca gag ccc cgt cca ctg cag
     303  Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln
     304           275                    280                    285
E--> 306  gaa aga tgg gtc ggg ctg ccc ccc aac att gag gct gcg gca gtg tca
     307  Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser
     308           290                    295                    300
E--> 310  ttg aat gat gga gat ttc tac ttc ttc aaa ggg ggt cga tgc tgg agg
     311  Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg
     312  305                    310                    315                    320
E--> 314  ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag ctg tgc cgg gca
     315  Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala
     316                    325                    330                    335
E--> 318  ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc ttc cct cct ctg
     319  Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu
     320                    340                    345                    350
E--> 322  cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac gtg ctg gcc cga
     323  Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg
     324                    355                    360                    365
E--> 326  ggg gga ctg caa gtg gag ccc tac tac ccc cga agt ctg cag gac tgg
     327  Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp
     328           370                    375                    380
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/050,216

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF3\02062002\J050216.raw

```
E--> 330  gga ggc atc cct gag gag gtc agc ggc gcc ctg ccg agg ccc gat ggc
     331  Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly
     332  385                 390             395              .400
E--> 334  tcc atc atc ttc ttc cga gat gac cgc tac tgg cgc ctc gac cag gcc
     335  Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala
     336                 405                 410              415
E--> 338  aaa ctg cag gca acc acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg
     339  Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp
     340  .               420             425              430
E--> 342  atg ggc tgc tgg cat gcc aac tcg ggg agc gcc ctg ttc
     343  Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu Phe
     344                 435             440              445
     391  <210> SEQ ID NO: 6
     392  <211> LENGTH: 471
     393  <212> TYPE: PRT
     394  <213> ORGANISM: Homo sapiens
     396  <400> SEQUENCE: 6
     397  Met His Pro Gly Val Leu Ala Ala Phe Leu Phe Leu Ser Trp Thr His
     398  1               5               10              15
     399  Cys Arg Ala Leu Pro Leu Pro Ser Gly Gly Asp Glu Asp Asp Leu Ser
     400                 20              25              30
     401  Glu Glu Asp Leu Gln Phe Ala Glu Arg Tyr Leu Arg Ser Tyr Tyr His
     402                 35              40              45
     403  Pro Thr Asn Leu Ala Gly Ile Leu Lys Glu Asn Ala Ala Ser Ser Met
     404          50              55              60
     405  Thr Glu Arg Leu Arg Glu Met Gln Ser Phe Phe Gly Leu Glu Val Thr
     406  65              70              75              80
     407  Gly Lys Leu Asp Asp Asn Thr Leu Asp Val Met Lys Lys Pro Arg Cys
     408                 85              90              95
     409  Gly Val Pro Asp Val Gly Glu Tyr Asn Val Phe Pro Arg Thr Leu Lys
     410                 100             105             110
     411  Trp Ser Lys Met Asn Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp
     412          115             120             125
     413  Met Thr His Ser Glu Val Glu Lys Ala Phe Lys Lys Ala Phe Lys Val
     414          130             135             140
     415  Trp Ser Asp Val Thr Pro Leu Asn Phe Thr Arg Leu His Asp Gly Ile
     416  145             150             155             160
     417  Ala Asp Ile Met Ile Ser Phe Gly Ile Lys Glu His Gly Asp Phe Tyr
     418                 165             170             175
     419  Pro Phe Asp Gly Pro Ser Gly Leu Leu Ala His Ala Phe Pro Pro Gly
     420                 180             185             190
     421  Pro Asn Tyr Gly Gly Asp Ala His Phe Asp Asp Asp Glu Thr Trp Thr
     422          195             200             205
     423  Ser Ser Ser Lys Gly Tyr Asn Leu Phe Leu Val Ala Ala His Glu Phe
     424          210             215             220
     425  Gly His Ser Leu Gly Leu Asp His Ser Lys Asp Pro Gly Ala Leu Met
     426  225             230             235             240
     427  Phe Pro Ile Tyr Thr Tyr Thr Gly Lys Ser His Phe Met Leu Pro Asp
     428                 245             250             255
```

insert
Notes

```
429  Asp Asp Val Gln Gly Ile Gln Ser Leu Tyr Gly Pro Gly Asp Glu Asp
430          260           265           270
431  Pro Asn Pro Lys His Pro Lys Thr Pro Asp Lys Cys Asp Pro Ser Leu
432          275           280           285
433  Ser Leu Asp Ala Ile Thr Ser Leu Arg Gly Glu Thr Met Ile Phe Lys
434          290           295           300
435  Asp Arg Phe Phe Trp Arg Leu His Pro Gln Gln Val Asp Ala Glu Leu
436  305           310           315           320
437  Phe Leu Thr Lys Ser Phe Trp Pro Glu Leu Pro Asn Arg Ile Asp Ala
438          325           330           335
439  Ala Tyr Glu His Pro Ser His Asp Leu Ile Phe Ile Phe Arg Gly Arg
440          340           345           350
441  Lys Phe Trp Ala Leu Asn Gly Tyr Asp Ile Leu Glu Gly Tyr Pro Lys
442          355           360           365
443  Lys Ile Ser Glu Leu Gly Leu Pro Lys Glu Val Lys Lys Ile Ser Ala
444      370           375           380
445  Ala Val His Phe Glu Asp Thr Gly Lys Thr Leu Leu Phe Ser Gly Asn
446  385           390           395           400
447  Gln Val Trp Arg Tyr Asp Asp Thr Asn His Ile Met Asp Lys Asp Tyr
448          405           410           415
449  Pro Arg Leu Ile Glu Glu Asp Phe Pro Gly Ile Gly Asp Lys Val Asp
450          420           425           430
451  Ala Val Tyr Glu Lys Asn Gly Tyr Ile Tyr Phe Phe Asn Gly Pro Ile
452          435           440           445
453  Gln Phe Glu Tyr Ser Ile Trp Ser Asn Arg Ile Val Arg Val Met Pro
454      450           455           460
455  Ala Asn Ser Ile Leu Trp Cys
456  465           470
458  <211> LENGTH: 7 56
459  <212> TYPE: PRT
460  <213> ORGANISM: Homo sapiens
462  <223> OTHER INFORMATION: The X at positions 2-5 can be any amino acid.
464  <223> OTHER INFORMATION: The amino acid at position 7 can be as few as 21,
465        up to 25, amino acids, and the amino acid can be
466        any amino acid.
468  <223> OTHER INFORMATION: The X at positions 9-12 can be any amino acid.
470  <223> OTHER INFORMATION: The X at position 16 can be any amino acid.
472  <223> OTHER INFORMATION: The X at position 18 can be any amino acid.
474  <223> OTHER INFORMATION: The X at positions 21-22 can be any amino acid.
476  <223> OTHER INFORMATION: The X at positions 25-26 can be any amino acid.
478  <223> OTHER INFORMATION: The X at positions 27-28 can be any amino acid.
480  <223> OTHER INFORMATION: The amino acid at position 37 can be as few as 26,
481        up to 71, amino acids, and the amino acid can be
482        any amino acid.
484  <223> OTHER INFORMATION: The X at position 39 can be any amino acid.
486  <223> OTHER INFORMATION: The X at position 42 can be any amino acid.
488  <223> OTHER INFORMATION: The X at position 48 can be any amino acid.
490  <223> OTHER INFORMATION: The amino acid at position 50 can be as few as 4,
491        up to 8, amino acids, and the amino acid can be
```

(handwritten annotations): valid; m5; Error; Summary Sheet; <210> 7 insert this mandatory numeric identifier and response; <220> insert this whenever <221>, <222>, or <223> is present; >28-29; e5 er; 28-29 what about Xaa at position 35?; item5; see p.5

RAW SEQUENCE LISTING   DATE: 02/06/2002
PATENT APPLICATION: US/10/050,216   TIME: 19:11:09

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF3\02062002\J050216.raw

```
        492      any amino acid.
        494 <223> OTHER INFORMATION: The X at position 52 can be any amino acid.
      · 496
E--> 496 <400> SEQUENCE: 7
W--> 497 Leu Xaa Xaa Xaa Xaa Tyr Xaa Gln Xaa Xaa Xaa Xaa Leu Pro Val Xaa
     498   1               5                  10                  15
W--> 499 Gly Xaa Leu Asp Xaa Xaa Thr Leu Xaa Xaa Met Xaa Xaa Pro Arg Cys
     500              20              25              30
W--> 501 Gly Val Xaa Asp Xaa Phe Xaa Gly Gly Xaa Leu Ala His Ala Phe Xaa
     502         35          40              45
W--> 503 Pro Xaa Gly Xaa Ala His Phe Asp
E--> 504  50
E-  508 <210> SEQ ID NO: 8
```

(handwritten annotations) 55 ← number the amino acids under every 5 = amino acids.

(handwritten) DO NOT use TAB codes between the numbers; use space characters

(handwritten) OK

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/050,216

DATE: 02/06/2002

TIME: 19:11:10

Input Set : **A:\SEQUENCE LISTING.txt**

Output Set: **N:\CRF3\02062002\J050216.raw**

```
L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:234 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:3
M:254 Repeated in SeqNo=3
L:496 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:496 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:6 differs:7
L:497 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:497 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:497 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:499 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:499 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:499 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:501 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:501 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:501 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:503 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:503 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:503 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:504 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:504 M:252 E: No. of Seq. differs, <211>LENGTH:Input:7 Found:56 SEQ:0
L:508 M:214 E: (33) Seq.# missing, SEQ ID NO:7
```